

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.  
Lal, Preeti  
Corley, Neil C.  
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN CITRATE SYNTHASE HOMOLOG
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0425 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 466 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: ENDCNOT03
  - (B) CLONE: 2171653

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Leu | Leu | Thr | Ala | Ala | Ala | Arg | Leu | Leu | Gly | Thr | Lys | Asn | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Cys | Leu | Val | Leu | Ala | Ala | Arg | His | Ala | Ser | Ala | Ser | Ser | Thr | Asn |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Lys | Asp | Ile | Leu | Ala | Asp | Leu | Ile | Pro | Lys | Glu | Gln | Ala | Arg | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Thr | Phe | Arg | Gln | Gln | His | Gly | Lys | Thr | Val | Val | Gly | Gln | Ile | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Asp | Met | Met | Tyr | Gly | Gly | Met | Arg | Gly | Met | Lys | Gly | Leu | Val | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Glu | Thr | Ser | Val | Leu | Asp | Pro | Asp | Glu | Gly | Ile | Arg | Phe | Arg | Gly | Phe |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser | Ile | Pro | Glu | Cys | Gln | Lys | Leu | Leu | Pro | Lys | Ala | Lys | Gly | Gly | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Pro | Leu | Pro | Glu | Gly | Leu | Phe | Trp | Leu | Leu | Val | Thr | Gly | His | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Pro | Thr | Glu | Glu | Gln | Val | Ser | Trp | Leu | Ser | Lys | Glu | Trp | Ala | Lys | Arg |  |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Ala | Ala | Leu | Pro | Ser | His | Val | Val | Thr | Met | Leu | Asp | Asn | Phe | Pro | Thr |  |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |  |
| Asn | Leu | His | Pro | Met | Ser | Gln | Leu | Ser | Ala | Ala | Val | Thr | Ala | Leu | Asn |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ser | Glu | Ser | Asn | Phe | Ala | Arg | Ala | Tyr | Ala | Gln | Gly | Ile | Ser | Arg | Thr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Lys | Tyr | Trp | Glu | Leu | Ile | Tyr | Glu | Asp | Ser | Met | Asp | Leu | Ile | Ala | Lys |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Pro | Cys | Val | Ala | Ala | Lys | Ile | Tyr | Arg | Asn | Leu | Tyr | Arg | Glu | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ser | Gly | Ile | Gly | Ala | Ile | Asp | Ser | Asn | Leu | Asp | Trp | Ser | His | Asn | Phe |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Thr | Asn | Met | Leu | Gly | Tyr | Thr | Asp | His | Gln | Phe | Thr | Glu | Leu | Thr | Arg |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Leu | Tyr | Leu | Thr | Ile | His | Ser | Asp | His | Glu | Gly | Gly | Asn | Val | Ser | Ala |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| His | Thr | Ser | His | Leu | Val | Gly | Ser | Ala | Leu | Ser | Asp | Pro | Tyr | Leu | Ser |  |
|     |     | 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |  |
| Phe | Ala | Ala | Ala | Met | Asn | Gly | Leu | Ala | Gly | Pro | Leu | His | Gly | Leu | Ala |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Asn | Gln | Glu | Val | Leu | Val | Trp | Leu | Thr | Gln | Leu | Gln | Lys | Glu | Val | Gly |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Lys | Asp | Val | Ser | Asp | Glu | Lys | Leu | Arg | Asp | Tyr | Ile | Trp | Asn | Thr | Leu |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Asn | Ser | Gly | Arg | Val | Val | Pro | Gly | Tyr | Gly | His | Ala | Val | Leu | Arg | Lys |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Thr | Asp | Pro | Arg | Tyr | Thr | Cys | Gln | Arg | Glu | Phe | Ala | Leu | Lys | His | Leu |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Pro | Asn | Asp | Pro | Met | Phe | Lys | Leu | Val | Ala | Gln | Leu | Tyr | Lys | Ile | Val |  |
|     | 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |  |
| Pro | Asn | Val | Leu | Leu | Glu | Gln | Gly | Lys | Ala | Lys | Asn | Pro | Trp | Pro | Asn |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Val | Asp | Ala | His | Ser | Gly | Val | Leu | Leu | Gln | Tyr | Tyr | Gly | Met | Thr | Glu |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Met | Asn | Tyr | Tyr | Thr | Val | Leu | Phe | Gly | Val | Ser | Arg | Ala | Leu | Gly | Val |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Leu | Ala | Gln | Leu | Ile | Trp | Ser | Arg | Ala | Leu | Gly | Phe | Pro | Leu | Glu | Arg |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Pro | Lys | Ser | Met | Ser | Thr | Glu | Gly | Leu | Met | Lys | Phe | Val | Asp | Ser | Lys |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |

Ser Gly  
465

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDCNOT03
- (B) CLONE: 2171653

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| CGCCGGTTTCG | TCTACTCTTT | CCTTCAGCCG | CCTCCTTTCA | ACCTTGTCAA | CCCCTCGGCG  | 60   |
| CGGCCTCTGG  | TGCAGCGGCG | GCGGCTCCTG | TTCCTGCCGC | AGCTCTCTCC | CTTTCTTACC  | 120  |
| TCCCCACCAG  | ATCCCGGAGA | TCGCCCGCCA | TGGCTTTACT | TACTGCGGCC | GCCCCGCTCT  | 180  |
| TGGGAACCAA  | GAATGCATCT | TGTCTTGTTT | TTGCAGCCCG | GCATGCCAGT | GCTTCCTCCA  | 240  |
| CGAATTTGAA  | AGACATATTG | GCTGACCTGA | TACCTAAGGA | GCAGGCCAGA | ATTAAGACTT  | 300  |
| TCAGGCAGCA  | ACATGGCAAG | ACGGTGCTGG | GCCAAATCAC | TGTGGACATG | ATGTATGGTG  | 360  |
| GCATGAGAGG  | CATGAAGGGA | TTGGTCTATG | AAACATCAGT | TCTTGATCCT | GATGAGGGCA  | 420  |
| TCCGTTTCCG  | AGGCTTTAGT | ATCCCTGAAT | GCCAGAAACT | GCTACCCAAG | GCTAAGGGTG  | 480  |
| GGGAAGAACC  | CCTGCCTGAG | GGCTTATTTT | GGCTGCTGGT | AACTGGACAT | ATCCCAACAG  | 540  |
| AGGAACAGGT  | ATCTTGGCTC | TCAAAAGAGT | GGGCAAAGAG | GGCAGCTCTG | CCTTCCCATG  | 600  |
| TGGTCACCAT  | GCTGGACAAC | TTTCCCACCA | ATCTACACCC | CATGTCTCAG | CTCAGTGCAG  | 660  |
| CTGTTACAGC  | CCTCAACAGT | GAAAGTAACT | TTGCCCGAGC | ATATGCACAG | GGTATCAGCC  | 720  |
| GAACCAAGTA  | CTGGGAGTTG | ATTTATGAAG | ACTCTATGGA | TCTAATCGCA | AAGCTACCTT  | 780  |
| GTGTTGCAGC  | AAAGATCTAC | CGAAATCTCT | ACAGAGAAGG | CAGCGGTATT | GGGGCCATTG  | 840  |
| ACTCTAACCT  | GGACTGGTCT | CACAATTTC  | CCAACATGTT | AGGCTATACT | GATCATCAGT  | 900  |
| TCACTGAGCT  | CACGCGCCTG | TACCTCACCA | TCCACAGTGA | CCATGAGGGT | GGCAATGTAA  | 960  |
| GTGCCCATAC  | CAGCCATTTG | GTGGGCAGTG | CCCTTTCCGA | CCCTTACCTG | TCCTTTGCAG  | 1020 |
| CAGCCATGAA  | CGGGCTGGCA | GGGCCTCTCC | ATGGACTGGC | AAATCAGGAA | GTGCTTGTCT  | 1080 |
| GGCTAACACA  | GCTGCAGAAG | GAAGTTGGCA | AAGATGTGTC | AGATGAGAAG | TTACGAGACT  | 1140 |
| ACATCTGGAA  | CACACTCAAC | TCAGGACGGG | TTGTTCCAGG | CTATGGCCAT | GCAGTACTAA  | 1200 |
| GGAAGACTGA  | TCCGCGATAT | ACCTGTCAGC | GAGAGTTTGC | TCTGAAACAC | CTGCCTAATG  | 1260 |
| ACCCCATGTT  | TAAGTTGGTT | GCTCAGCTGT | ACAAGATTGT | GCCCAATGTC | CTCTTAGAGC  | 1320 |
| AGGGTAAAGC  | CAAGAATCCT | TGGCCCAATG | TAGATGCTCA | CAGTGGGGTG | CTGCTCCAGT  | 1380 |
| ATTATGGCAT  | GACGGAGATG | AATTACTACA | CGGTCTCTGT | TGGGGTGTC  | CGAGCATTGG  | 1440 |
| GTGTACTGGC  | ACAGCTCATC | TGGAGCCGAG | CCTTAGGCTT | CCCTCTAGAA | AGGCCCCAAGT | 1500 |
| CCATGAGCAC  | AGAGGGTCTG | ATGAAGTTTG | TGGACTCTAA | GTGAGGGTAA | AACTGGAGAC  | 1560 |
| TGGGTGAAAG  | TGACTACCA  | AAAGTGAGGA | AGCCTAAATA | AAAAGTATAC | TTTTTGTTTCA | 1620 |
| GGGGGCCTTT  | AAAGACTTAA | GATTAAATTA | TATCTGAGGC | ACTGATAATA | TGTTTGAGGT  | 1680 |
| TAAAATATAA  | ATTAAGACTT | TAAAAGATGA | AAAATGGTCC | CTTCTTCCCT | AATCAGCTCC  | 1740 |
| CTTCCCCTGC  | CTGGTATGAG | TTGCCCATCA | TACGCATGGT | CCTGGAGGAT | GACCAGGACT  | 1800 |
| AATGCATGTG  | GTATGAGTAG | GTTTGGCCCC | CTCACTATCT | CTAGAGTGAG | AATCTGGCTC  | 1860 |
| CTGTTTCCAT  | GGGTCAAAGC | CGGTTGCAGA | GAATCTGTAG | TCACTTTGGA | GCTTTAGCTT  | 1920 |
| CTCTGCCAAG  | CCCTCAATAA | GCCAGCAAAC | CAGGACTCTG | CCCTTCTGT  | TTCCATAGGA  | 1980 |
| ATCATGTTGG  | ATAGTCAGCT | GTACCAAGCC | CCTTGGCCCT | CTCCCATGCA | CACAAACACC  | 2040 |
| TCCTAGCAAG  | ACCTGTTGGT | TAGCTGGACA | TGCTTTGGCA | ATTTTTTTAT | ACTACCAAGT  | 2100 |
| GACCATATTG  | GCATGGCATT | TTTTGGTGAT | G          |            |             | 2131 |

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GenBank  
(B) CLONE: 164419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ala Leu Leu Thr Ala Ala Ala Arg Leu Phe Gly Ala Lys Asn Ala
1      5      10      15
Ser Cys Leu Val Leu Ala Ala Arg His Ala Ser Ala Ser Ser Thr Asn
20      25      30
Leu Lys Asp Ile Leu Ala Asp Leu Ile Pro Lys Glu Gln Ala Arg Ile
35      40      45
Lys Thr Phe Arg Gln Gln His Gly Asn Thr Val Val Gly Gln Ile Thr
50      55      60
Val Asp Met Met Tyr Gly Gly Met Arg Gly Met Lys Gly Leu Val Tyr
65      70      75      80
Glu Thr Ser Val Leu Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Tyr
85      90      95
Ser Ile Pro Glu Cys Gln Lys Met Leu Pro Lys Ala Lys Gly Gly Glu
100     105     110
Glu Pro Leu Pro Glu Gly Leu Phe Trp Leu Leu Val Thr Gly Gln Ile
115     120     125
Pro Thr Glu Glu Gln Val Ser Trp Leu Ser Lys Glu Trp Ala Lys Arg
130     135     140
Ala Ala Leu Pro Ser His Val Val Thr Met Leu Asp Asn Phe Pro Thr
145     150     155     160
Asn Leu His Pro Met Ser Gln Leu Ser Ala Ala Ile Thr Ala Leu Asn
165     170     175
Ser Glu Ser Asn Phe Ala Arg Ala Tyr Ala Glu Gly Ile His Arg Thr
180     185     190
Lys Tyr Trp Glu Leu Ile Tyr Glu Asp Cys Met Asp Leu Ile Ala Lys
195     200     205
Leu Pro Cys Val Ala Ala Lys Ile Tyr Arg Asn Leu Tyr Arg Glu Gly
210     215     220
Ser Ser Ile Gly Ala Ile Asp Ser Lys Leu Asp Trp Ser His Asn Phe
225     230     235     240
Thr Asn Met Leu Gly Tyr Thr Asp Ala Gln Phe Thr Glu Leu Met Arg
245     250     255
Leu Tyr Leu Thr Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala
260     265     270
His Thr Ser His Leu Val Gly Ser Ala Leu Ser Asp Pro Tyr Leu Ser
275     280     285
Phe Ala Ala Ala Met Asn Gly Leu Ala Gly Pro Leu His Gly Leu Ala
290     295     300
Asn Gln Glu Val Leu Val Trp Leu Thr Gln Leu Gln Lys Glu Val Gly
305     310     315     320
Lys Asp Val Ser Asp Glu Lys Leu Arg Asp Tyr Ile Trp Asn Thr Leu
325     330     335
Asn Ser Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
340     345     350
Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu Phe Ala Leu Lys His Leu
355     360     365
Pro His Asp Pro Met Phe Lys Leu Val Ala Gln Leu Tyr Lys Ile Val
370     375     380
Pro Asn Val Leu Leu Glu Gln Gly Lys Ala Lys Asn Pro Trp Pro Asn
385     390     395     400
Val Asp Ala His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Met Thr Glu

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PF-0425-1 DIV

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Met | Asn | Tyr | Tyr | Thr | Val | Leu | Phe | Gly | Val | Ser | Arg | Ala | Leu | Gly | Val |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Leu | Ala | Gln | Leu | Ile | Trp | Ser | Arg | Ala | Leu | Gly | Phe | Pro | Leu | Glu | Arg |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Pro | Lys | Ser | Met | Ser | Thr | Asp | Gly | Leu | Ile | Lys | Leu | Val | Asp | Ser | Lys |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |